I claim:

1. A method of amplifying a target nucleic acid sequence, the method comprising,

(a) mixing a set of primers with a target sample, to produce a primer-target sample mixture, and incubating the primer-target sample mixture under conditions that promote hybridization between the primers and the target sequence in the primer-target sample mixture,

(b) mixing DNA polymerase with the primer-target sample mixture, to produce a polymerase-target sample mixture, and incubating the polymerase-target sample mixture under conditions that promote replication of the target sequence,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand.

2. The method of claim 1 wherein the target sequence comprises an amplification target and a hybridization target, wherein the hybridization target flanks the amplification target,

wherein the set of primers comprises a plurality of primers,

wherein each primer comprises a complementary portion, wherein the complementary portions of the primers are each complementary to a different portion of the hybridization target.

3. The method of claim 1 wherein step (b) further comprises incubating the polymerase-target sample mixture under conditions that promote strand displacement.

4. The method of claim 1 wherein the set of primers has 3 or more primers.

5. The method of claim 4 wherein the set of primers has 4 or more primers.

6. The method of claim 5 wherein the set of primers has 5 or more primers.

7. The method of claim 1 wherein the conditions that promote replication of the target sequence are substantially isothermic.

8. The method of claim 1 wherein the conditions that promote replication of the target sequence do not involve thermal cycling.

9. The method of claim 1 wherein step (b) does not include thermal cycling.

10. The method of claim 2 wherein the set of primers comprises a right set of primers and a left set of primers,

wherein the target sequence is double-stranded, having a first and a second strand,

wherein the hybridization target comprises a right and left hybridization target, wherein the right hybridization target flanks the amplification target on one end and the left hybridization target flanks the amplification target on the other end,

wherein the complementary portions of the right set primers are (i) all complementary to the first strand of the target sequence and (ii) each complementary to a different portion of the right hybridization target, and

wherein the complementary portions of the left set primers are (i) all complementary to the second strand of the target sequence and (ii) each complementary to a different portion of the left hybridization target.

11. The method of claim 10 wherein the right and left set of primers each have 3 or more primers.

12. The method of claim 11 wherein the right and left set of primers each have 4 or more primers.

13. The method of claim 12 wherein the right and left set of primers each have 5 or more primers.

14. The method of claim 10 wherein the right and left set of primers each have the same number of primers.

15. The method of claim 1 wherein the target sequence is a nucleic acid sample of substantial complexity, and wherein the set of primers comprises primers having random nucleotide sequences.

16. The method of claim 15 wherein the target sequence is a sample of genomic nucleic acid.

17. The method of claim 15 wherein the primers are from 12 to 60 nucleotides in length.

18. The method of claim 17 wherein the primers are from 12 to 40 nucleotides in length.

19. The method of claim 18 wherein the primers are from 15 to 40 nucleotides in length.

20. The method of claim 19 wherein the primers are from 15 to 25 nucleotides in length.

21. The method of claim 15 wherein the primers are all of the same length.

22. The method of claim 15 wherein each primer comprises a constant portion and a random portion, wherein the constant portion of each primer has the same nucleotide sequence and the random portion of each primer has a random nucleotide sequence.

23. The method of claim 1 wherein the target sequence is concatenated DNA.

24. The method of claim 23 wherein the concatenated DNA is concatenated with linkers.

25. The method of claim 24 wherein each linker comprises a primer complement portion, wherein each primer comprises a complementary portion,

wherein the complementary portion of each primer is complementary to the complementary portion of the linkers.

26. The method of claim 23 wherein the set of primers comprises primers having random nucleotide sequences.

27. The method of claim 26 wherein each primer comprises a constant portion and a random portion, wherein the constant portion of each primer has the same nucleotide sequence and the random portion of each primer has a random nucleotide sequence.

28. The method of claim 23 wherein the concatenated DNA is formed by ligating DNA fragments together.

29. The method of claim 28 wherein the DNA fragments are cDNA made from mRNA.

30. The method of claim 29 wherein the mRNA comprises a mixture of mRNA isolated from cells.

31. The method of claim 1 wherein the target sequence is not a nucleic acid molecule made up of multiple tandem repeats of a single sequence that was synthesized by rolling circle replication.

32. A kit for amplifying a target nucleic acid sequence wherein the target sequence comprises an amplification target and a hybridization target, wherein the hybridization target flanks the amplification target, the kit comprising

a set of primers wherein the set of primers comprises a plurality of primers, wherein each primer comprises a complementary portion, wherein the complementary portions of the primers are each complementary to a different portion of the hybridization target, and

a strand displacing DNA polymerase or a DNA polymerase and a compatible strand displacement factor.

33. The kit of claim 32 wherein the target sequence is double-stranded,

having a first and a second strand,

wherein the hybridization target comprises a right and left hybridization target, wherein the right hybridization target flanks the amplification target on one end and the left hybridization target flanks the amplification target on the other end,

wherein the set of primers comprises a right set of primers and a left set of primers,

wherein the complementary portions of the right set primers are (i) all complementary to the first strand of the target sequence and (ii) each complementary to a different portion of the right hybridization target, and

wherein the complementary portions of the left set primers are (i) all complementary to the second strand of the target sequence and (ii) each complementary to a different portion of the left hybridization target.

32. A kit for amplifying a target nucleic acid sequence wherein the target sequence is a nucleic acid sample of substantial complexity, the kit comprising

a set of primers wherein the set of primers comprises primers having random nucleotide sequences, and

a strand displacing DNA polymerase or a DNA polymerase and a compatible strand displacement factor.